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## RAW SEQUENCE LISTING

DATE: 03/21/2002

PATENT APPLICATION: US/10/025,335

TIME: 14:05:16

Input Set : N:\Crif3\RULE60\10025335.raw

Output Set: N:\CRF3\03212002\J025335.raw

## SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
5   (i) APPLICANT: Coleman, Roger
6       Bandman, Olga
8   (ii) TITLE OF INVENTION: NOVEL HUMAN C5A-LIKE RECEPTOR
10  (iii) NUMBER OF SEQUENCES: 3
12  (iv) CORRESPONDENCE ADDRESS:
13      (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
14      (B) STREET: 3174 Porter Drive
15      (C) CITY: Palo Alto
16      (D) STATE: CA
17      (E) COUNTRY: USA
18      (F) ZIP: 94304
20  (v) COMPUTER READABLE FORM:
21      (A) MEDIUM TYPE: Diskette
22      (B) COMPUTER: IBM Compatible
23      (C) OPERATING SYSTEM: DOS
24      (D) SOFTWARE: FastSEQ for Windows Version 2.0
26  (vi) CURRENT APPLICATION DATA:
C--> 27      (A) APPLICATION NUMBER: US/10/025,335
C--> 28      (B) FILING DATE: 18-Dec-2001
29      (C) CLASSIFICATION:
31  (vii) PRIOR APPLICATION DATA:
32      (A) APPLICATION NUMBER: 08/791,974
33      (B) FILING DATE:
35  (viii) ATTORNEY/AGENT INFORMATION:
36      (A) NAME: Billings, Lucy J.
37      (B) REGISTRATION NUMBER: 36,749
38      (C) REFERENCE/DOCKET NUMBER: PF-0198 US
40  (ix) TELECOMMUNICATION INFORMATION:
41      (A) TELEPHONE: 415-855-1555
42      (B) TELEFAX: 415-845-4166
43      (C) TELEX
46  (2) INFORMATION FOR SEQ ID NO: 1:
48      (i) SEQUENCE CHARACTERISTICS:
49          (A) LENGTH: 319 amino acids
50          (B) TYPE: amino acid
51          (C) STRANDEDNESS: single
52          (D) TOPOLOGY: linear
54      (vii) IMMEDIATE SOURCE:
55          (A) LIBRARY: Consensus
56          (B) CLONE: 346874
58      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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ENTERED

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60 Met Thr Asn Ser Ser Phe Phe Cys Pro Val Tyr Lys Asp Leu Glu Pro
61 1 5 10 15
62 Phe Thr Tyr Phe Phe Tyr Leu Val Phe Leu Val Gly Ile Ile Gly Ser
63 20 25 30
64 Cys Phe Ala Thr Trp Ala Phe Ile Gln Lys Asn Thr Asn His Arg Cys
65 35 40 45
66 Val Ser Ile Tyr Leu Ile Asn Leu Leu Thr Ala Asp Phe Leu Leu Thr
67 50 55 60
68 Leu Ala Leu Pro Val Lys Ile Val Val Asp Leu Gly Val Ala Pro Trp
69 65 70 75 80
70 Lys Leu Lys Ile Phe His Cys Gln Val Thr Ala Cys Leu Ile Tyr Ile
71 85 90 95
72 Asn Met Tyr Leu Ser Ile Ile Phe Leu Ala Phe Val Ser Ile Asp Arg
73 100 105 110
74 Cys Leu Gln Leu Thr His Ser Cys Lys Ile Tyr Arg Ile Gln Glu Pro
75 115 120 125
76 Gly Phe Ala Lys Met Ile Ser Thr Val Val Trp Leu Met Val Leu Leu
77 130 135 140
78 Ile Met Val Pro Asn Met Met Ile Pro Ile Lys Asp Ile Lys Glu Lys
79 145 150 155 160
80 Ser Asn Val Gly Cys Met Glu Phe Lys Lys Glu Phe Gly Arg Asn Trp
81 165 170 175
82 His Leu Leu Thr Asn Phe Ile Cys Val Ala Ile Phe Leu Asn Phe Ser
83 180 185 190
84 Ala Ile Ile Leu Ile Ser Asn Cys Leu Val Ile Arg Gln Leu Tyr Arg
85 195 200 205
86 Asn Lys Asp Asn Glu Asn Tyr Pro Asn Val Lys Lys Ala Leu Ile Asn
87 210 215 220
88 Ile Leu Leu Val Thr Thr Gly Tyr Ile Ile Cys Phe Val Pro Tyr His
89 225 230 235 240
90 Ile Val Arg Ile Pro Tyr Thr Leu Ser Gln Thr Glu Val Ile Thr Asp
91 245 250 255
92 Cys Ser Thr Arg Ile Ser Leu Phe Lys Ala Lys Glu Ala Thr Leu Leu
93 260 265 270
94 Leu Ala Val Ser Asn Leu Cys Phe Asp Pro Ile Leu Tyr Tyr His Leu
95 275 280 285
96 Ser Lys Ala Phe Arg Ser Lys Val Thr Glu Thr Phe Ala Ser Pro Lys
97 290 295 300
98 Thr Lys Ala Gln Lys Glu Lys Leu Arg Cys Glu Asn Asn Ala
99 305 310 315

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101 (2) INFORMATION FOR SEQ ID NO: 2:

103 (i) SEQUENCE CHARACTERISTICS:

104 (A) LENGTH: 1257 base pairs

105 (B) TYPE: nucleic acid

106 (C) STRANDEDNESS: single

107 (D) TOPOLOGY: linear

109 (vii) IMMEDIATE SOURCE:

110 (A) LIBRARY: Consensus

111 (B) CLONE: 346874

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113      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
115 CAGCTCATGC TTCTCTGAAG ACTTGCAGCA AGGCTTGCTG AGGCTCACAG AAGATAGCCC      60
116 CAGTGTTTTG GAGTGGTTTT GAATGTGATT CTGAGATCAG ACTGACTGAG CTGGAATCCT      120
117 GGCTTTATAT CTTACCAGCT ACWCAACCTT GGAGTCTTAG AAATTTTTTTC ITTTCARTAA      180
118 GCAGTCATCC TTACTTTCCC TCAAGATGAC AAACAGTTCG TTCTTCTGCC CAGTTTATAA      240
119 AGATCTGGAG CCATTCACGT ATTTTITTTA TTTAGTTTTT CTTGTTGGAA TTATTGGAAG      300
120 TTGTTTTGCA ACCTGGGCTT TTATACAGAA GAATACGAAT CACAGGTGTG TGAGCATCTA      360
121 CTTAATTAAT TTGCTTACAG CCGATTTCCCT GCTTACTCTG GCATTACCAG TGAAAATTGT      420
122 TGTTGACTTG GGTGTGGCAC CTTGGAARCT GAAGATATTC CACTGCCAAG TAACAGCCTG      480
123 CCTCATCTAT ATCAATATGT ATTTATCAAT TATCTTCTTA GCATTTGTCA GCATTGACCG      540
124 CTGTCTTCAG CTGACACACA GCTGCAAGAT CTACCGAATA CAAGAACCCG GGTTTGCCAA      600
125 AATGATATCA ACCGTTGTGT GGCTAATGGT CCTTCTTATA ATGGTGCCAA ATATGATGAT      660
126 TCCCATCAAA GACATCAAGG AAAAGTCAAA TGTGGGTTGT ATGGAGTTTA AAAAGGAATT      720
127 TGGAAGAAAT TGGCATTTCG TGACAAATTT CATATGTGTA GCAATATTTT TAAATTTCTC      780
128 AGCCATCATT TTAATATCCA ATTGCCTTGT AATTCGACAG CTCTACAGAA ACAAAGATAA      840
129 TGAAAATTAC CCAAATGTGA AAAAGGCTCT CATCAACATA CTTTTAGTGA CCACGGGCTA      900
130 CATCATATGC TTTGTTTCCTT ACCACATTGT CCGAATCCCG TATACCCTCA GCCAGACAGA      960
131 AGTCATAACT GATTGCTCAA CCAGGATTTT ACTCTTCAAA GCCAAAGAGG CTACACTGCT      1020
132 CCTGGCIGTG TCGAACCTGT GCTTTGATCC TATCCTGTAC TATCACCTCT CAAAAGCATT      1080
133 CCGCTCAAAG GTCACGTAGA CTTTTCCTTC ACCTAAAGAG ACCAAGGCTC AGAAAGAAAA      1140
134 ATTAAGATGT GAAAATAATG CATAAAAGAC AGGATTTTTT GTGCTACCAA TTCTGGCCTT      1200
135 ACTGGACCAT AAAGTTAATT ATAGCTTTGA AAGATAAAAA AAAAAAAAAA AAAAAAA      1257

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## (2) INFORMATION FOR SEQ ID NO: 3:

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139      (i) SEQUENCE CHARACTERISTICS:
140          (A) LENGTH: 350 amino acids
141          (B) TYPE: amino acid
142          (C) STRANDEDNESS: single
143          (D) TOPOLOGY: linear
145      (vii) IMMEDIATE SOURCE:
146          (A) LIBRARY: GenBank
147          (B) CLONE: 115262
149      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
151 Met Asn Ser Phe Asn Tyr Thr Thr Pro Asp Tyr Gly His Tyr Asp Asp
152 1      5      10      15
153 Lys Asp Thr Leu Asp Leu Asn Thr Pro Val Asp Lys Thr Ser Asn Thr
154      20      25      30
155 Leu Arg Val Pro Asp Ile Leu Ala Leu Val Ile Phe Ala Val Val Phe
156      35      40      45
157 Leu Val Gly Val Leu Gly Asn Ala Leu Val Val Trp Val Thr Ala Phe
158      50      55      60
159 Gln Ala Lys Arg Thr Ile Asn Ala Ile Trp Phe Leu Asn Leu Ala Val
160      65      70      75
161 Ala Asp Phe Leu Ser Cys Leu Ala Leu Pro Ile Leu Phe Thr Ser Ile
162      80      85      90
163 Val Gln His His His Trp Pro Phe Gly Gly Ala Ala Cys Ser Ile Leu
164      100     105     110
165 Pro Ser Leu Ile Leu Leu Asn Met Tyr Ala Ser Ile Leu Leu Leu Ala
166      115     120     125
167 Thr Ile Ser Ala Asp Arg Phe Leu Leu Val Phe Lys Pro Ile Trp Cys

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168      130      135      140
169 Gln Asn Phe Arg Gly Ala Gly Leu Ala Trp Ile Ala Cys Ala Val Ala
170 145      150      155      160
171 Trp Gly Leu Ala Leu Leu Leu Thr Ile Pro Ser Phe Leu Tyr Arg Val
172      165      170      175
173 Val Arg Glu Glu Tyr Phe Pro Pro Lys Val Leu Cys Gly Val Asp Tyr
174      180      185      190
175 Ser His Asp Lys Arg Arg Glu Arg Ala Val Ala Ile Val Arg Leu Val
176      195      200      205
177 Leu Gly Phe Leu Trp Pro Leu Leu Thr Leu Thr Ile Cys Tyr Thr Phe
178      210      215      220
179 Ile Leu Leu Arg Thr Trp Ser Arg Arg Ala Thr Arg Ser Thr Lys Thr
180 225      230      235      240
181 Leu Lys Val Val Val Ala Val Val Ala Ser Phe Phe Ile Phe Trp Leu
182      245      250      255
183 Pro Tyr Gln Val Thr Gly Ile Met Met Ser Phe Leu Glu Pro Ser Ser
184      260      265      270
185 Pro Thr Phe Leu Leu Leu Asn Lys Leu Asp Ser Leu Cys Val Ser Phe
186      275      280      285
187 Ala Tyr Ile Asn Cys Cys Ile Asn Pro Ile Ile Tyr Val Val Ala Gly
188      290      295      300
189 Gln Gly Phe Gln Gly Arg Leu Arg Lys Ser Leu Pro Ser Leu Leu Arg
190 305      310      315      320
191 Asn Val Leu Thr Glu Glu Ser Val Val Arg Glu Ser Lys Ser Phe Thr
192      325      330      335
193 Arg Ser Thr Val Asp Thr Met Ala Gln Lys Thr Gln Ala Val
194      340      345      350

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\03212002\J025335.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:28 M:220 C: Keyword misspelled or invalid format. [(B) FILING DATE:]